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- SKEWED/SLANTED IMAGES
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- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:15:24 ; Search time 1951.49 Seconds  
(without alignments)  
11875.950 Million cell updates/sec

Title: US-09-576-424-11  
Perfect score: 1431  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

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2: em_esthum:*
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8: em_htc:*
9: gb_est1:*
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11: gb_htc:*
12: gb_est3:*
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16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	63.0	1020	14	BQ062878
2	864	60.4	947	14	BQ709771
3	850.4	59.4	958	14	BQ706140
4	842.4	58.9	926	12	BG755166
5	832	58.1	988	14	BQ708857
6	831.2	58.1	901	13	BM007892

7	824.4	57.6	1029	14	BQ063185
8	822.8	57.5	887	14	BQ711255
9	822.2	57.5	918	14	BQ708022
10	818.6	57.2	995	14	BM914540
11	808.8	56.5	881	14	BQ711291
12	800.2	55.9	1031	14	BQ064886
13	797.4	55.7	936	14	BQ711727
14	796	55.6	940	14	BQ705928
15	787.4	55.0	977	14	BQ710532
16	786.4	55.0	980	14	BM914504
17	785.2	54.9	843	13	BM007897
18	778.8	54.4	991	14	BQ708936
19	777.2	54.3	973	14	BQ706204
20	776	54.2	930	13	BM007597
21	770.6	53.9	981	14	BM914528
22	764.6	53.4	926	14	BQ710304
23	764.2	53.4	917	14	BQ708169
24	759.4	53.1	961	14	BQ710233
25	756.6	52.9	945	14	BQ712403
26	752.4	52.6	1012	14	BM914556
27	750.6	52.5	895	14	BQ708303
28	750.4	52.4	783	13	BM007838
29	748	52.3	1026	14	BM914288
30	741.4	51.8	914	14	BQ712363
31	737.4	51.5	913	14	BQ707472
32	734.2	51.3	906	14	BQ711709
33	733.8	51.3	944	14	BQ712397
34	733.6	51.3	919	14	BQ709339
35	732.8	51.2	936	14	BQ707530
36	732.4	51.2	855	13	BM007689
37	731.8	51.1	1014	14	BM914505
38	730.4	51.0	973	14	BQ708902
39	729.6	51.0	888	12	BG757604
40	728.8	50.9	941	14	BQ712021
41	728.6	50.9	925	14	BQ709853
42	728.4	50.9	991	14	BQ707621
43	726.8	50.8	870	12	BG757815
44	726.2	50.7	925	14	BQ709152
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#### ALIGNMENTS

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DEFINITION AGENCOURT_6826949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
5', mRNA sequence.
ACCESSION  BQ062878
VERSION    BQ062878.1
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1020)
AUTHORS   NIH-MGC http://mgc.mci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094 row: h column: 21
            High quality sequence start: 21
            High quality sequence stop: 681.
            Location/Qualifiers

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#### FEATURES

[illegible]







Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2464 row: c column: 02  
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Location/Qualifiers

## FEATURES

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/db\_xref="taxon:9606"  
/clone="IMAGE:6277561"  
/lab host="NIH MGC 113"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."  
230 a 338 c 258 g 162 t

## BASE COUNT

ORIGIN

Query Match 58.1%; Score 832; DB 14; Length 988;  
Best Local Similarity 94.7%; Pred. No. 3e-201;  
Matches 905; Conservative 0; Mismatches 45; Indels 6; Gaps 4;

QY 393 CTGGTTCGATGTCCTGGGCGCGGAGTCCTGGTCAACCGTCTCTCAGCTAGCACCAGGG 452  
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QY 453 CCCATCGGTCTCCCGCTGGACCCCTCTCCAAAGAGCCTCTGGGGGACAGCGGCCCT 512  
DB 65 CCCATCGGTCTCCCGCTGGACCCCTCTCCAAAGAGCCTCTGGGGGACAGCGGCCCT 124  
QY 513 GGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACTCAGGGCG 572  
DB 125 GGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACTCAGGGCG 184  
QY 573 CTGACACGCGCGGTGCACACCTTCCCGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCT 632  
DB 185 CTGACACGCGCGGTGCACACCTTCCCGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCT 244  
QY 633 CAGCAGCGTGGTACCGTCCCTCAGCAGCTTGGGCCACCCAGACCTACATCTGCAAGCT 692  
DB 245 CAGCAGCGTGGTACCGTCCCTCAGCAGCTTGGGCCACCCAGACCTACATCTGCAAGCT 304  
QY 693 GAATCACAAGCCGACCAACCAAGTGGACAAAGAGCAGAGCCCAATCTTGTGACAA 752  
DB 305 GAATCACAAGCCGACCAACCAAGTGGACAAAGAGTGGACCAATCTTGTGACAA 364  
QY 753 AACTCACAATGCCACCGTCCCGGACCACTGAATCTCTGGGGGACCGTCACTTCTCT 812  
DB 365 AACTCACAATGCCACCGTCCCGGACCACTGAATCTCTGGGGGACCGTCACTTCTCT 424  
QY 813 CTTTCCCCCAAAACCAAGGACACCGTCTATGATCTCCCGGACCCCTGAGGTCAATGCT 872  
DB 425 CTTTCCCCCAAAACCAAGGACACCGTCTATGATCTCCCGGACCCCTGAGGTCAATGCT 484  
QY 873 GGTGTGGACGTGAGCCAGAGACCTTGAGTCAAGTTCAGTCTGAGTGGACGGGT 932  
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QY 1173 GGTACGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGCAGCATCGCGTGGAGTGGGA 1232  
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QY 1289 ACGGC-TCCTTCTTCTCTACAGCAAGCTCACCCTGGGACAGAGCAGGTGGCAGCA 1343  
DB 904 ACGGCTTCTTCTTCTCTACAGAAAGCTCCCGGGGGAACAAAGCAGGAGGTGGCA 959

## RESULT 6

BM007892

LOCUS

DEFINITION 60361757F1 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:5450611 5',  
mRNA sequence.

ACCESSION

BM007892

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 901)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM1939 row: j column: 20  
High quality sequence stop: 834.

## FEATURES

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/organism="Homo sapiens"  
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/lab host="NIH MGC 113"  
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209 a 315 c 234 g 143 t

## BASE COUNT

ORIGIN

Query Match 58.1%; Score 831.2; DB 13; Length 901;  
Best Local Similarity 97.7%; Pred. No. 4.6e-201;  
Matches 864; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

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Qy	468	CCTGGCACCCCTCTCTCCAAAGAGCACCTCTGGGGGGCACAGCGGCCCTCGGCTGCCCTGGTCAA	527
Db	79	CCTGGCACCCCTCTCTCCAAAGAGCACCTCTGGGGGCACAGAGCCCTGGGCTGCCCTGGTCAA	138
Qy	528	GGACTACTTCCCCGAAACCGGTGACGGTGTCTGTGAACTCAGAGGCCCTCTGACAGCGGCGT	587
Db	139	GGACTACTTCCCCGAAACCGGTGACGGTGTCTGTGAACTCAGAGGCCCTCTGACAGCGGCGT	198
Qy	588	GCACACCTTCCCGGCTGCTCTACAGTCCCTCAGAGACTCTACTCCCTCAGCAGCGTGTGTAC	647
Db	199	GCACACCTTCCCGGCTGCTCTACAGTCCCTCAGAGACTCTACTCCCTCAGCAGCGTGTGTAC	258
Qy	648	CGTGCCCTCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAACTCAAGGCCAG	707
Db	259	CGTGCCCTCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAACTCAAGGCCAG	318
Qy	708	CAACACCAAGGTGACAAGAAAGCAGAGGCCCAAACTCTTGTGACAAAACCTCACACATGCC	767
Db	319	CAACACCAAGGTGACAAGAAAGTGAAGCCCAAACTCTTGTGACAAAACCTCACACATGCC	378
Qy	768	ACCGTGCCAGCACCTGAACTCTCTGGGGGACCGTCACTCTCTCTCTTCCCCCCTCAAAACC	827
Db	379	ACCGTGCCAGCACCTGAACTCTCTGGGGGACCGTCACTCTCTCTCTTCCCCCCTCAAAACC	438
Qy	828	CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGTGTGAGCGTGTAG	887
Db	439	CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGTGTGAGCGTGTAG	498
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Db	499	CCACGAAGACCCCTGAGGTCAAGTTCAACTGTGTAGTGTGAGGTGAGGTGATATGC	558
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ACCESSION GENEID: 1029 bp Homo sapiens cdna clone IMAGE:5924769  
VERSION BQ063185.1 GI:19890681  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.



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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: i column: 20
High quality sequence stop: 667.

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EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 208 a 316 c 245 g 147 t 2 others
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Best Local Similarity 95.4%; Pred. No. 9.2e-199;
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QY 458 CGGTCTTCCCTTGGGCGCGGAGTCTCTCAGGAGCAGTCTGGGCGCAGCGGCGCTGGCT 517
DB 61 CGGTCTTCCCTTGGGCGCGGAGTCTCTCAGGAGCAGTCTGGGCGCAGCGGCGCTGGCT 120

QY 518 GCTGTGTCAGGAGTACTTCCCGGAAACCGGTGACGGTGTCTGGGAACTCAGGCGGCGCTGA 577
DB 121 GCTGTGTCAGGAGTACTTCCCGGAAACCGGTGACGGTGTCTGGGAACTCAGGCGGCGCTGA 180

QY 578 CCAGCGGCGTGCACACTTCCCGGCTGCTTACAGTCTCTCAGGACTCTACTCTCTCAGCA 637
DB 181 CCAGCGGCGTGCACACTTCCCGGCTGCTTACAGTCTCTCAGGACTCTACTCTCTCAGCA 240

QY 638 GCGTGTGTGACCGTGGCGCTCCAGCAGTCTGGGCAACCCAGACCTACATCTCAACGTGAATC 697
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QY 698 ACAAGCCGAGCAACACCAAGGTGGACAGAAAGAGCAGAGCCCAAAATCTTGTGACAAATCT 757
DB 301 ACAAGCCGAGCAACACCAAGGTGGACAGAAAGGTGGAGCCCAAAATCTTGTGACAAATCT 360

QY 758 ACACATGCCCGTGGCGGCGGAGTCTGTAACCTCTGGGCGGAGCGTCAAGTCTCTCTTCC 817
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QY 818 CCCCAGGAGCCAGGAGCAGCCTCATGATCTCCCGGACCCCTCAGGAGTCAATCGTGGTGG 877
DB 421 CCCCAGGAGCCAGGAGCAGCCTCATGATCTCCCGGACCCCTCAGGAGTCAATCGTGGTGG 480

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QY 1296 CTTCTTCT 1304
DB 901 GTCTTTCT 909

RESULT 10
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ACCESSION BM914540
VERSION BM914540.1 GI:19364919
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 995)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: 1 column: 16
High quality sequence stop: 718.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480223"
/clone_lib="NIH_MGC_113"
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a

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BASE COUNT      241 a 330 c 259 g 165 t
ORIGIN
Query Match      57.2%; Score 818.6; DB 14; Length 995;
Best Local Similarity 96.0%; Pred. No. 7.9e-198;
Matches 861; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
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Db 1 AACTTCTACTTTGACGATTTGGGGCCAGGAAACGCTGTCACCGTCTCTCAGCTCCACC 60
QY 448 AAGGGCCCATCGCTTTCCTCCCTGGCAGCACCCTCTCCAGAGCACCTCTGGGGGACAGCG 507
Db 61 AAGGGCCCATCGCTTTCCTCCCTGGCAGCACCCTCTCCAGAGCACCTCTGGGGGACAGCG 120
QY 508 GCCCTGGGCTGCTGCTGCTCAAGACTACTTTCCTCCGAAACCGGTGACGGTGTCTGGAAC 567
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QY 628 TCCCTCAGCAGCGTGTGACCGTGCCTCCAGAGCTTGGGCACCCAGACTACATCTGC 687
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QY 688 AACGTGAATCACAAGCCAGCAACCAAGGTGGCAAGAAAGCAGAGCCCAATCTGT 747
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DEFINITION AGENCOURT_8347186 NIH_MGC_113 Homo sapiens.cDNA clone IMAGE:6279096
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ACCESSION      BQ711291
VERSION        BQ711291.1
KEYWORDS       GI:21850190
SOURCE         human.
ORGANISM       Homo sapiens
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REFERENCE
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL         Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: c9apbs-r@mail.nih.gov
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Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2468 row: c column: 01
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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BASE COUNT      220 a 285 c 237 g 139 t
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QY 792 GGGGGGACCGTCACTCTCTCTCCCGCAAAACCCAAAGGACACCTCATGATCTCCCG 851
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REFERENCE   1 (bases 1 to 936)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone Distribution: MGC clone distribution information can be
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             into EcoRI/XhoI sites using the following 5' adaptor:
             GGCACGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."
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Db 250 ACACCTCTATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGTGAGACGTGAGCCAG 309
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QY 953 CAAAGCCGGGAGGAGCAGTACAAACAGCAGCTACCGTGTGTGTGAGCGTCTCACCGTCC 1012
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VERSION    B0705928.1  GI:21844827
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SOURCE     human.
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 940)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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             GGCACGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
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SOURCE     human.
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REFERENCE  
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.TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 977)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILLNL at:  
<http://image.llnl.gov>  
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into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
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QY 835 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCTGCTGGTGGTGGAGCGTGAACCGAA 894  
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QY 895 GACCTGAGTCAAGTTCAACTGTGACGCGCGGTGGAGGTGCAATATGCCAAGACA 954  
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GenCore version 5.1.6  
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6	1251.6	87.5	1596	9	AK098516	AK098516 Homo sapi
7	1236.8	86.4	1589	9	AK057775	AK057775 Homo sapi
8	1224.8	85.6	1418	6	A49389	A49389 Sequence 7
9	1213.6	84.8	1418	6	AR176296	AR176296 Sequence
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11	1181	82.5	1404	6	AR135375	AR135375 Sequence
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13	1176.2	82.2	1404	6	AR135376	AR135376 Sequence
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35	1121.2	78.4	1617	6	A29585	A29585 H.sapiens c
36	1116.2	78.0	1624	9	HSIGGILH	Y14735 Homo sapien
37	1115.6	78.0	1359	9	MACIGHVCDR	L13307 Macaca fasc
38	1114	77.8	1631	9	AK097010	AK097010 Homo sapi
39	1112.4	77.7	1437	6	AR108865	AR108865 Sequence
40	1112	77.7	1666	9	BC006402	BC006402 Homo sapi
41	1108.2	77.4	1628	9	AK097361	AK097361 Homo sapi
42	1107.6	77.4	1633	9	AK097367	AK097367 Homo sapi
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44	1103.8	77.1	1668	9	BC026038	BC026038 Homo sapi
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ALIGNMENTS

RESULT 1	AR108867	Sequence 11 from patent US 6113898.	1431 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR108867	Sequence 11 from patent US 6113898.	1431 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	AR108867	Sequence 11 from patent US 6113898.	1431 bp	DNA	linear	PAT 14-FEB-2001
ACCESSION	AR108867	Sequence 11 from patent US 6113898.	1431 bp	DNA	linear	PAT 14-FEB-2001
VERSION	AR108867.1	GI:12825143	1431 bp	DNA	linear	PAT 14-FEB-2001
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1431)					
AUTHORS	Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.					
TITLE	Human B7.1-specific primatized antibodies and transfectomas					
JOURNAL	expressing said antibodies					
	Patent: US 6113898-A 11 05-SEP-2000;					





Db 606 CCGACACCGGTGACGGTGTCTGTAAGTCTAGGCGCCTGACAGCGCGGTGCACACCTTC 665  
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Db 666 CCGGCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCC 725  
QY 658 AGCAGCTTGGGACCCAGACCTTACATCTGCAAGCTGAATCAGAGCCGACACCAAG 717  
Db 726 AGCAGCTTGGGACCCAGACCTTACATCTGCAAGCTGAATCAGAGCCGACACCAAG 785  
QY 718 GTGGACAAGAAAGCAGACCCCAATCTGTGCAAAACTCACAATGCCACCGTCCCA 777  
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QY 838 CTCATGATCTCCCGGACCCCTGAGGTCAATGCTGCTGCTGAGCTGAGCCACGAAGAC 897  
Db 906 CTCATGATCTCCCGGACCCCTGAGGTCAATGCTGCTGCTGAGCTGAGCCACGAAGAC 965  
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Db 1386 ACCGTGGACAAGAGAGTGGCAGCAGGGGAAAGTCTTCTCATGCTCCGCTGATGATGAG 1445  
QY 1378 GCTCTGACAACACATACAGGAGAGAGCTTCTCCTGTCTCCGGGTAAATGA 1431  
Db 1446 GCTCTGACAACACATACAGAGAGAGCTTCTCCTGTCTCCCGGTAAATGA 1499

## RESULT 4

E10697  
LOCUS 1431 bp RNA linear PAT 29-SEP-1997  
DEFINITION cDNA encoding heavy chain of human monoclonal antibody against human cytomegalovirus 65kD antigen.  
ACCESSION E10697  
VERSION E10697.1 GI:22027790  
KEYWORDS JP 1996038178-A/20.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1431)  
AUTHORS Tanaka,S., Niwa,H. and Tanaka,H.

TITLE HUMAN MONOCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR CLONING OF GENE THEREOF  
JOURNAL Patent: JP 1996038178-A 20 13-FEB-1996;  
TANAKA HIDEYUKI, NISSHINBO IND INC  
COMMENT OS Homo sapiens (human)  
PN JP 1996038178-A/20  
PD 13-FEB-1996  
PF 20-FEB-1995 JP 1995030742  
PI 18-FEB-1994 JP 94P 21628  
PI TANAKA SHIGEKI, NIWA HIRONUKI, TANAKA HIDEYUKI PC  
C12N15/09,C07K16/08,C12N1/21,C12N15/02,C12P21/08,C12Q1/68, PC  
G01N33/53,  
PC G01N33/531,G01N33/577,(C12N1/21,C12R1:19),(C12P21/08, PC  
C12R1:19);  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
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Db      415  ACCCTGGTACCGCTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCACCC 474
QY      478  TCTCTCAAGAGCACTCTGGGGGACAGGGCCCTGGGCTGCTGTGTCAGAGACTACTTTC 537
Db      475  TCTCTCAAGAGCACTCTGGGGGACAGGGCCCTGGGCTGCTGTGTCAGAGACTACTTTC 534
QY      538  CCGGAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACAGCGCGTGCACACTTC 597
Db      535  CCGGAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACAGCGCGTGCACACTTC 594
QY      598  CCGGCTGTCTCAGTCTCAGGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCC 657
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QY      658  AGCAGTTGGGACCCAGACCTTACATCTGCAAGCTGAATCAAGCCCAAGCAACCAAG 717
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Db      715  GTGGACAAGAAAGTTCAGGCCCAATCTTGTGCAAACTCACATGCCCCACCGTGCCCA 774
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QY      1378  GCTCTGCAACAACATACACGAGAGAGCCCTCTCCCTGTCTCCGGTAAATGA 1431
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RESULT 5

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DEFINITION      Ig gamma immunoglobulin heavy chain.
ACCESSION      AK057754
VERSION      AK057754.1 GI:16553681
KEYWORDS      oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens cersbellum cDNA to mRNA, clone_cbl: CBL01928.
ORGANISM      Homo sapiens
REFERENCE      1 Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
AUTHORS      Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M.,
      Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
      Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
      Sugano, S.
      NEDO human cDNA sequencing project
      Unpublished
      2 (bases 1 to 1594)
      Sugano, S. and Suzuki, Y.
      Direct Submission
      Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
      University of Tokyo, Laboratory of Genome Structure, Human Genome
      Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
      (E-mail: cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
      Fax:81-3-5449-5416)
COMMENT      NEDO human cDNA sequencing project supported by Ministry of
      Economy, Trade and Industry of Japan; cDNA full insert sequencing:
      Research Association for Biotechnology (RAB); cDNA library
      construction and 5'-end one pass sequencing: Institute of Medical
      Science, University of Tokyo, Laboratory of Genome Structure, Human
      Genome Center; 3'-end one pass sequencing: RAB; clone selection for
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Best Local Similarity 93.8%; Pred. No. 7.1e-244;
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RESULT 6  
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LOCUS  
DEFINITION Homo sapiens cDNA FLJ25650 fis, clone SYN01104, highly similar to Ig gamma -immunoglobulin heavy chain.  
ACCESSION AK098516  
VERSION AK098516.1 GI:21758543  
KEYWORDS oligo capping; fjs (full insert sequence).  
SOURCE Homo sapiens synovial membrane (knee) cDNA to mRNA, clone\_lib:SYN clone:SYN01104.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Ishibaashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuka,T., Hiraoka,S., Murakawa,K., Tanai,H., Ishida,M., Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Nakagawa,K., Mizuno,S., Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1596)  
Sugano,S. and Suzuki,Y.  
Direct Submission  
Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.  
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ACCESSION AK057775  
VERSION AK057775.1 GI:16553709  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1  
Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,  
Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M.,  
Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,  
Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and  
Sugano, S.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1589)  
Sugano, S. and Suzuki, Y.  
Direct Submission  
Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure, Human Genome  
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
Fax:81-3-5449-5416)  
NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction and 5'-end one pass sequencing: Institute of Medical  
Science, University of Tokyo, Laboratory of Genome Structure, Human  
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DEFINITION Sequence 7 from patent US 6312690.  
ACCESSION ARI176296  
VERSION ARI176296.1 GI:17918651  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1418)  
AUTHORS Edelman,L., Margartite,C., Kaczorek,M. and Chaabihi,H.  
TITLE Monoclonal recombinant anti-rhesus D (D7C2) antibody  
JOURNAL Patent: US 6312690-A 7 06-NOV-2001;  
FEATURES  
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Query Match 84.8%; Score 1213.6; DB 6; Length 1418;  
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[illegible]

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LOCUS	AR135375	1404 bp	DNA linear PAT 16-JUN-2001
DEFINITION	Sequence 7 from patent US 6136310.		
ACCESSION	AR135375		
VERSION	AR135375.1	GI:14476047	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1404)		
AUTHORS	Hanna, N., Newman, R. Anthony. and Reff, M. Elliot.		
TITLE	Recombinant anti-CD4 antibodies for human therapy		
JOURNAL	Patent: US 6136310-A 7 24-OCT-2000;		
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DEFINITION Sequence 11 from patent US 6136310.  
ACCESSION AR135377  
VERSION AR135377.1 GI:14476049  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1404)  
AUTHORS Hanna N., Newman, R. Anthony, and Reff, M. Elliot.  
TITLE Recombinant anti-CD4 antibodies for human therapy  
JOURNAL Patent: US 6136310-A 11 24-OCT-2000;

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DEFINITION Sequence 9 from patent US 6136310.
ACCESSION AR135376
VERSION AR135376.1 GI:14476048
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Hanna, N., Newman, R., Anthony, and Reff, M., Elliot.
TITLE Recombinant anti-CD4 antibodies for human therapy
JOURNAL Patent: US 6136310-A 9 24-OCT-2000;
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DB 121 TGCAGTGTCTCTGTGGTCTCCATCAGCGGTGATTAATTGGTTCTGGATCCGCCAGTCC 180
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 QY 1381 CTGCAACACCTACACGAGAGAGAGCTTCTCCTCTGCTCCGGGTAATGA 1431  
 Db 1354 CTGCAACACCTACACAGAGAGAGCTTCTCCTCTGCTCCGGGTAATGA 1404

## RESULT 14

BC024289  
 LOCUS 1630 bp mRNA linear PRI 28-FEB-2002  
 DEFINITION Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA, complete cds.

ACCESSION BC024289  
 VERSION BC024289.1 GI:18999464  
 KEYWORDS MGC.

## SOURCE

Homo sapiens.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1630)

## AUTHORS

Strausberg, R.

## TITLE

Direct Submission

## JOURNAL

Submitted (26-FEB-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 42 Row: 0 Column: 20

This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF

analysis, Genomescan gene prediction, Similarity but not identity

to protein.

## FEATURES

Location/Qualifiers

1..1630

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/db\_xref="taxon:9606"

/clone="MGC:39273 IMAGE:5440834"

/tissue type="Spleen"

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/lab\_host="DH10B-R"

/note="Vector: pOTB7"

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## CDS

VKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS  
 VNHALHHNYTKSLSLSPGK"  
 BASE COUNT 374 a 518 c 442 g 296 t  
 ORIGIN

Query Match 79.8%; Score 1142.6; DB 9; Length 1630;  
 Best Local Similarity 88.5%; Pred. No. 8.4e-221;  
 Matches 1267; Conservative 0; Mismatches 149; Indels 15; Gaps 2;

QY 1 ATGAAACACCTGTGGTCTTCTCCTCTGCTGGGAGCTCCAGATGCTGCTGCTCCAG 60  
 Db 64 ATGGAACCTGGGCTCGCTGGGTTTCTTGTGCTATTTTGAAGGTCTCCAGTGTGAG 123  
 QY 61 GTGAGCTGTCAGAGTTCGGGCCAGAGACTGTGGAAGCCCTTCGGAGACCTGTCCCTCACC 120  
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 QY 121 TCGCTGTCTGTGGTCTCCATCAGCGGTGTTATGCTGGGGCTGGAGTCCGCCAGCCC 180  
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 QY 181 CCAGGAAGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240  
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Db 1271 CCGTGTGGACTCCGACGGCTCCTTCTCTACAGCAAGCTCACCGTGGACAAGACA 1330  
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QY 1394 ACACGCAGAAAGCCCTCTCCCTCTCTCCGGTAAATGA 1431  
Db 1391 ACACGCAGAAAGCCCTCTCCCTCTCTCCGGTAAATGA 1428

Search completed: June 3, 2003, 17:50:57  
Job time : 3717.97 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 319.784 Seconds  
(without alignments)  
10077.457 Million cell updates/sec

Title: US-09-576-424-11  
Perfect score: 1431  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	18	Primitised anti-hu
2	1431	100.0	1431	19	Macaque primatized
3	1431	100.0	1431	24	DNA sequence of a
4	1315.8	91.9	1431	18	Primitised anti-hu
5	1315.8	91.9	1431	19	Macaque primatized
6	1315.8	91.9	1431	24	DNA sequence of a
7	1276.4	89.2	1567	22	Human immune syste
8	1261.2	88.1	1431	17	Monoclonal antibod
9	1261	88.1	1634	21	Human immune syste

10	1224.8	85.6	1418	17	AAT26889	Anti-rhesus D reco
11	1181	82.5	1404	18	AAT62868	Human gamma-4 heav
12	1177.8	82.3	1404	18	AAT62870	Human gamma-4PE he
13	1176.2	82.2	1404	18	AAT62869	Human gamma-4E hea
14	1151	80.4	1428	22	AAH74680	Nucleotide sequenc
15	1136.4	79.4	1428	18	AAT61241	Human anti-RSV mon
16	1134	79.2	1430	24	AAK98701	cDNA of the heavy
17	1134	79.2	1644	22	AA525593	Human cDNA encodin
18	1133.8	79.2	1507	21	AAA09695	Human immunoglobul
19	1133.4	79.2	1798	21	AA098220	Human colon cancer
20	1123.6	78.5	1428	18	AAT61279	Human anti-RSV mon
21	1122.8	78.5	1599	24	ABK64550	Human benign prost
22	1122.8	78.5	1599	24	ABL62673	Colon adenocarcino
23	1122.8	78.5	1599	24	ABL65479	Lung cancer relate
24	1122.8	78.5	1599	24	ABL66294	Lung cancer relate
25	1121.2	78.4	1617	14	AAQ35099	Antibody D heavy c
26	1120.8	78.3	19035	19	AAV61794	Traget plasmid Man
27	1119.6	78.2	1549	13	AAQ20066	Encodes heavy chai
28	1119	78.2	1442	22	AA084208	Plasmid Glambda-1B
29	1118	78.1	1449	20	AA086951	Monoclonal antibod
30	1118	78.1	1449	20	AA086952	Monoclonal antibod
31	1115.8	78.0	6281	22	AA084206	Plasmid Glambda-1A
32	1112.4	77.7	1437	19	AAV35487	Macaque primatized
33	1112.4	77.7	1437	24	AS17245	DNA sequence of a
34	1110.8	77.6	1427	19	AAV41429	Plasmid Hui9Hcpod
35	1110.8	77.6	1427	19	AAV41431	Plasmid Hui9Hcpod
36	1110.8	77.6	1437	18	AA113847	Primatized anti-hu
37	1109.8	77.6	1458	13	AAQ23571	Reshaped CD4 antib
38	1109.8	77.6	1458	13	AAQ23581	Plasmid Hui9Hcpod
39	1109.2	77.5	1427	19	AAV41432	Reshaped CD4 antib
40	1107.8	77.4	1576	14	AAQ49944	Human anti-HBs hea
41	1102.8	77.1	6284	19	AAV41427	Plasmid Hui9Hcpod
42	1102.2	77.0	6557	17	AA115932	Anti-IgE VH expres
43	1101	76.9	1431	22	AA091017	Chimeric 4H6 anti-
44	1101	76.9	1431	22	AA091018	Chimeric 4H6 anti-
45	1100.8	76.9	2912	22	AA522718	Human cDNA encodin

## ALIGNMENTS

RESULT 1  
AAT62513  
ID AAT62513 standard; DNA; 1431 BP.  
XX AC  
XX AAT62513;  
XX AC  
XX 25-MAY-1997 (first entry)

XX Primitised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.  
XX Monoclonal antibody; cynomolgus monkey; macaque; 16C10;  
XX Primitised antibody; B7 antigen; CD28; immunosuppressive;  
XX autoimmune disease; idiopathic thrombocytopenia purpura;  
XX systemic lupus erythematosus; rheumatoid arthritis; psoriasis;  
XX type 1 diabetes mellitus; graft versus host disease;  
XX hetero-hybridoma; transfectoma; ss.  
XX Chimeric Macaca cynomolgus;  
XX Chimeric Homo sapiens.

XX WO9640878-A1.  
XX PD 19-DEC-1996.  
XX PF 06-JUN-1996; 96WO-US10053.  
XX PR 07-JUN-1995; 95US-0487550.  
XX PA (IDEC-) IDEC PHARM CORP.  
XX PI Anderson DR, Brans P, Hanna N, Shestowsky WS;  
XX







AAS17247 standard; DNA; 1431 BP.
AAS17247;
12-MAR-2002 (first entry)
DNA sequence of a primatised form of the heavy chain of 16C10 antibody.
Human; macaque monkey; light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
Chimeric - Homo sapiens. Chimeric - Macaca sp. Synthetic.
Key Location/Qualifiers
CDS 1..1431 /*tag= a /product= "Heavy chain of 16C10 antibody"
WO200189567-A1.
29-NOV-2001.
22-MAY-2001; 2001WO-US16364.
22-MAY-2000; 2000US-0576424.
(IDEC-) IDEC PHARM CORP.
Anderson DR, Hanna N, Brans P;
WPI; 2002-089895/12.
P-PSDB; AAU11646.
Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as allergy
Example 8; Fig 5b; 89pp; English.
The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the heavy chain of 16C10, a primatised antibody used in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2).
Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
Query Match 100.0%; Score 1431; DB 24; Length 1431;
Best Local Similarity 100.0%; Pred No. 8.5e-286;
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAAACACCTGTGGTTTCTTCCTCCCTGGTGCGAGCTCCCAGATGGGTCCTGTGCCAG 60











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QY 238 TACAACCCCTCCTCAAGAGTCAAGTCAACATTTCAACAGACACGTCACGAACCAAGTTC 297
Db 315 TACAACCCCTCCTCAAGAGTCAAGTCAACATTTCAACAGACACGTCACGAACCAAGTTC 374
QY 298 TCCTGGAAGCTGAACCTCTATGACCGCGGACACAGCGCGTGTATTACTGTGTGAGAGAT 357
Db 375 TCCTGGAAGCTGAGCTCTGTGACTGCGGACAGACAGCGCGTGTATTACTGTGCGAGAGA- 433
QY 358 CGCTCTTTTTCAGTTGTTGGAATGTTTAAACAACACTGGTTCGATGTCTGGGCGCCGGGA 417
Db 434 -----TGACGTAGTTTAAAGGGGGGGAACACTACGCTATGGAAGTCTGTGGGCGCAGGA 485
QY 418 GTCTCTGCTCAGCTCTCCTCAGCTAGCACCAAGGGCCCATCGTCTTCCCTCCCTGGCACCC 477
Db 486 ACCCTGGTCAACGCTCTCCTCAGCTCTCCTCAGCTCTCCTCAGCAAGGGCCCATCGTCTTCCCTCCCTGGCACCC 545
QY 478 TCTTCAAGAGACCTCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGCTCAAGACTACTTC 537
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QY 538 CCGGAAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAAGCGCGGTGCACACCTTC 597
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QY 598 CCGGCTGTCTCAGTCTCCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTGCCTCC 657
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QY 898 CTTGAGGTCAAGTTCAACTGTTGACGCGGCGTGGAGGTGCATTAATGCCAAGACAAAG 957
Db 966 CTTGAGGTCAAGTTCAACTGTTGACGCGGCGTGGAGGTGCATTAATGCCAAGACAAAG 1025
QY 958 CCGCGGGAGGAGGATPACAACAGCAGTACCGTGTGGTCAAGCTCTCTCAAGTCTGAC 1017
Db 1026 CCGCGGGAGGAGGATPACAACAGCAGTACCGTGTGGTCAAGCTCTCTCAAGTCTGAC 1085
QY 1018 CAGGACTGCTGAATGGCAAGGATCAAGTGCAGGCTCTCAACAAAGCCCTCCAGGC 1077
Db 1086 CAGGACTGCTGAATGGCAAGGATCAAGTGCAGGCTCTCAACAAAGCCCTCCAGGC 1145
QY 1078 CCGATCGAGAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACCAAGGTGTACACC 1137
Db 1146 CCGATCGAGAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACCAAGGTGTACACC 1205
QY 1138 CTGCCCCCATTCGCGGATGAGTGCACAAAGACCAAGTCAAGCTGACCTGCTGTGCAAA 1197
Db 1206 CTGCCCCCATTCGCGGAGGAGATGACCAAGAACCAAGTCAAGCTGACCTGCTGTGCAAA 1265
QY 1198 GCGCTTCTATCCAGACACATCCCGTGGAGTGGGAGCAATGGGCGAGGACCAAC 1257
Db 1266 GCGCTTCTATCCAGACACATCCCGTGGAGTGGGAGCAATGGGCGAGGACCAAC 1325
QY 1258 TACAAGACCAACGCTCTCCGCTGTGGAATCCGAGCGCTCTTCTTCTTACAGCAAGCTC 1317
Db 1326 TACAAGACCAACGCTCTCCGCTGTGGAATCCGAGCGCTCTTCTTCTTACAGCAAGCTC 1385
QY 1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGATGAG 1377
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Db 1386 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGATGAG 1445
QY 1378 GCTCTGCAACCACTACACGCAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
Db 1446 GCTCTGCAACCACTACACAGAGAGCCTCTCCCTGTCTCCCGGGTAAATGA 1499
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## RESULT 8

```
AAT18059
ID AAT18059 standard; DNA; 1431 BP.
XX
AC AAT18059;
XX
DT 16-AUG-1996 (first entry)
XX
DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
XX
KW Polymerase chain reaction; primer; amplify; PCR; light chain; Mab;
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1428
FT /tag= a
FT sig_peptide 1..57
FT /tag= b
FT mat_peptide 58..1425
FT /tag= c
FT 3'UTR 1426..1431
FT /tag= d
XX
PN JP08038178-A.
XX
PD 13-FEB-1996.
XX
PF 20-FEB-1995; 95JP-0030742.
XX
PR 18-FEB-1994; 94JP-0021628.
XX
PA (NISR) NISSHINBO IND INC.
PA (TANA/) TANAKA H.
XX
WI WI; 1996-154852/16.
DR P-PSDB; AAR93553.
XX
PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT produced by primer amplification, used in the diagnosis of hCMV
PT infection
XX
PS Claim 6; Page 16-18; 22pp; Japanese.
XX
CC The sequences given in AAT18059-60 encode the heavy and light chains
CC respectively of a monoclonal antibody against a 65 kD antigen of human
CC cytomegalovirus (hCMV). These sequences were amplified using the
CC sequences given in AAT18040-58. The monoclonal antibody may be used
CC in the diagnosis of hCMV.
XX
SQ Sequence 1431 BP; 314 A; 475 C; 379 G; 263 T; 0 other;
```

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Query Match 88.1%; Score 1261.2; DB 17; Length 1431;
Best Local Similarity 93.9%; Pred. No. 8.6e-251;
Matches 1347; Conservative 0; Mismatches 78; Indels 9; Gaps 3;
QY 1 ATGAACACCTGTGTGTTCTTCTCTCTCTGTGGCAGCTCCAGATGGGTCTCTGTCACG 60
Db 1 ATGAAGCATCTTGTGTTCTTCTCTCTCTGTGGGCGGTCCAGATGGGTCTCTGTCACG 60
QY 61 GTGCAAGTGCAGAGTCCGGGCCAGGACTGTGTGAAGCCTTCGAGACCCCTGTCCCTCACC 120
Db 61 CTGAGCTGCAGAGTCCGGGCCAGGACTGTGTGAAGCCTTCGAGACCCCTGTCCCTCACC 120
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AAAT62869	standard; DNA; 1404 BP.
XX	AC AAT62869;
XX	18-OCT-1997 (first entry)
XX	Human gamma-4E heavy chain DNA.
XX	CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
XX	cytomegalus monkey; autoimmune disease; rheumatoid arthritis;
KW	leukemia; lymphoma; graft-versus-host disease; aschma;
KW	transplant rejection; HIV; therapy; CE9 gamma-4E; ss.
XX	Homo sapiens.
OS	WO9709351-A1.
XX	13-MAR-1997.
XX	05-SEP-1996; 96WO-US14324.
XX	06-SEP-1995; 95US-0523894.
PR	(IDEC-) IDEC PHARM CORP.
XX	Hanna N, Newman RA, Reff ME;
PI	WPI; 1997-201913/18.
XX	P-PSDB; AAW14926.
XX	Chimeric antibody comprising monkey variable domains and human
PT	constant domains - affects CD4-mediated immune functions, esp.
PT	useful for treatment of autoimmune disease, e.g. rheumatoid
XX	arthritis
XX	Disclosure; Page 86-88; 155pp; English.
XX	DNA sequences (AAT62868-70) respectively code for the heavy chain
CC	regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC	mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC	mutations. They can be used to provide novel monoclonal and
CC	chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC	gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC	combined with the antigen binding domains (see also AAW14922-23) of
CC	macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC	show high affinity to human CD4, have little or no immunogenicity
CC	in humans and show reduced or absence of effector function. The
CC	gamma-4E and -4PE mutations confer activity enhanced stability and
CC	eliminate depleting activity. The antibodies can be used to treat
CC	autoimmune diseases such as rheumatoid arthritis.
XX	Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;
XX	Query Match 82.2%; Score 1176.2; DB 18; Length 1404;
XX	Best Local Similarity 90.2%; Pred. No. 2.9e-233;
XX	Matches 1291; Conservative 0; Mismatches 113; Indels 27; Gaps 2
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Db	1 ATGAAACACCTGTGGTCTTCTCTCTCTGTGGGAGCTCCAGATGGGTCTGTGCCAG 60
Qy	61 GTGCAGCTGCAGGAGTGGGGCCCGAGACTGGTGAGCCCTTCGGAGACCTGTCCCTCAC 120
Db	61 GTGCAGCTGCAGGAGTGGGGCCCGAGACTGGTGAGCCCTTCGGAGACCTGTCCCTCAC 120
Qy	121 TGCCTGTCTCTGTGGGTCTCCATCAGCGGTGTATGGCTGGGGGTGGATCGCCAGGCC 180
Db	121 TGCAGTGTCTCTGTGGGTCTCCATCAGCGGTGTATGGCTGGGGGTGGATCGCCAGGCC 180
Qy	181 CCAGGGAGGGGGTGGAGTGGAGTTCCTATAGTAGTAGTGGGAACACCTACTAC 240





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Db |||||  
Qy 971 ACAACAGCAGTACCGTGTGGTCAGCGTCTCTCACCGTCTCTGCACACAGGACTGGCTGAATG 1030  
Db |||||  
Qy 1034 GCAAGGAGTACAAGTCAAGTCTCCAAACAAGCCCTCCAGCCCTCCATCGAGAAACCA 1093  
Db |||||  
Qy 1031 GCAAGGAGTACAAGTCAAGTCTCCAAACAAGCCCTCCAGCCCTCCATCGAGAAACCA 1090  
Db |||||  
Qy 1094 TCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGG 1153  
Db |||||  
Qy 1091 TCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGG 1150  
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Qy 1154 ATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCTGTCTCAAGGCTTCTATCCAGCG 1213  
Db |||||  
Qy 1151 ATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCTGTCTCAAGGCTTCTATCCAGCG 1210  
Db |||||  
Qy 1214 ACATGCGCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACCAACTACAAGACACGCTTC 1273  
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Qy 1211 ACATGCGCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACCAACTACAAGACACGCTTC 1270  
Db |||||  
Qy 1274 CCGTGTCTGACTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1333  
Db |||||  
Qy 1271 CCGTGTCTGACTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1330  
Db |||||  
Qy 1334 GGTGCGAGCAGGGGAAACGTCTTCTCATGTCTCGTGTATGATGAGGCTCTGCACACCACT 1393  
Db |||||  
Qy 1331 GGTGCGAGCAGGGGAAACGTCTTCTCATGTCTCGTGTATGATGAGGCTCTGCACACCACT 1390  
Db |||||  
Qy 1394 ACACGAGAAAGAGCTCTCCCTGTCTCCGGGTAATGA 1431  
Db |||||  
Qy 1391 ACACGAGAAAGAGCTCTCCCTGTCTCCGGGTAATGA 1428  
Db |||||

Search completed: June 3, 2003, 14:45:43  
Job time : 324.784 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 17:51:01 ; Search time 188.659 Seconds  
(without alignments)  
10227.493 Million cell updates/sec

Title: US-09-576-424-11

Perfect score: 1431  
Sequence: 1 atgaacacctgtggtttt.....ccctgtctccgggtaaaatga 1431

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

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14: /cgn2\_6/prodata/1/pubnpa/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1429.4	99.9	1431	9	US-10-073-138-6
4	1315.8	91.9	1431	9	US-10-124-905-3
5	1315.8	91.9	1431	9	US-09-948-4295-3
6	1314.2	91.8	1431	9	US-10-073-138-2
7	1181	82.5	1404	9	US-10-211-357-7
8	1177.8	82.3	1404	9	US-10-211-357-11
9	1176.2	82.2	1404	9	US-10-211-357-9
10	1134.8	79.3	1428	10	US-09-740-002-17
11	1133.4	79.2	1798	9	US-09-925-299-230
12	1133.4	79.2	1798	10	US-09-925-299-230
13	1125.2	78.6	1428	10	US-09-740-002-19
14	1122.8	78.5	1599	10	US-09-954-456-789
15	1122.8	78.5	1599	10	US-09-954-456-789
16	1118	78.1	1449	10	US-09-747-669-1
17	1118	78.1	1449	10	US-09-747-669-2
18	1112.4	77.7	1437	9	US-10-124-905-7
19	1112.4	77.7	1437	9	US-09-948-4295-7

20	1112.4	77.7	1437	9	US-10-073-138-4	Sequence 4, Appli
21	1110.8	77.6	1427	12	US-10-066-895-20	Sequence 20, Appl
22	1110.8	77.6	1427	12	US-10-066-895-25	Sequence 25, Appl
23	1109.2	77.5	1427	12	US-10-066-895-27	Sequence 27, Appl
24	1102.8	77.1	6284	12	US-10-066-895-14	Sequence 14, Appl
25	1100.4	76.9	1356	10	US-09-823-698A-27	Sequence 27, Appl
26	1100	76.9	1539	10	US-09-823-849A-87	Sequence 87, Appl
27	1098.2	76.7	1617	10	US-09-822-830A-571	Sequence 571, Appl
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29	1096.6	76.6	9209	9	US-09-911-703-3	Sequence 3, Appli
30	1096.6	76.6	9209	9	US-09-905-928-2	Sequence 2, Appli
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32	1096.6	76.6	18986	9	US-10-109-853-2	Sequence 2, Appli
33	1093.8	76.4	8120	9	US-09-726-258-68	Sequence 68, Appl
34	1091.8	76.3	9182	9	US-09-927-122-41	Sequence 41, Appl
35	1091.8	76.3	9182	9	US-09-927-121B-89	Sequence 89, Appl
36	1089.2	76.1	1347	10	US-09-736-371B-20	Sequence 20, Appl
37	1089	76.1	1404	10	US-09-825-012-10	Sequence 10, Appl
38	1089	76.1	1565	10	US-09-822-849A-104	Sequence 104, Appl
39	1088.6	76.1	1640	10	US-09-822-849A-321	Sequence 321, Appl
40	1088.4	76.1	1598	10	US-09-822-849A-103	Sequence 103, Appl
41	1086.4	75.9	2196	10	US-09-825-012-44	Sequence 44, Appl
42	1086.4	75.9	2196	10	US-09-825-012-45	Sequence 45, Appl
43	1086.4	75.9	2226	10	US-09-825-012-53	Sequence 53, Appl
44	1086.4	75.9	2226	10	US-09-825-012-54	Sequence 54, Appl
45	1086	75.9	1605	10	US-09-822-830A-501	Sequence 501, Appl

## ALIGNMENTS

### RESULT 1

US-10-124-905-11  
; Sequence 11, Application US/10124905  
; Patent No. US20020166136A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1431 base pairs







COUNTRY: USA  
 ZIP: 22314  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/124,905  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/383,916  
 FILING DATE:  
 APPLICATION NUMBER: US 08/487,550  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Teskin, Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-131  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1431 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1431  
 FEATURE:  
 NAME/KEY: mat\_peptide  
 LOCATION: 1..1431  
 US-10-124-905-3

Query Match 91.9%; Score 1315.8; DB 9; Length 1431;  
 Best Local Similarity 95.0%; Pred. No. 0;  
 Matches 1359; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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## RESULT 5

US-09-948-429B-3  
 ; Sequence 3, Application US/09948429B  
 ; Patent No. US20020177689A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Barrell R.  
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC









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## RESULT 8

US-10-211-357-11  
; Sequence 11, Application US/10211357  
; Publication No. US2003007725A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; Newman, Roland A.  
; Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/211.357  
; FILING DATE: 05-Aug-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/612,914A  
; FILING DATE: 10-Jul-2000  
; APPLICATION NUMBER: US 08/523,894  
; FILING DATE: 06-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1404 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and









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Db 1302 AGAACAGGTGAGCTGAGCTGCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGGTGG 1361  
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QY 1346 GGAACGTCTTCTATGCTCCGTGATGATGAGCTCTGCACAACTACACGCAAGA 1405  
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QY 1406 GCTCTCCCTGCTCCGGGTAAATGA 1431  
Db 1542 GCTCTCCCTGCTCCGGGTAAATGA 1567

## RESULT 13

US-09-740-002-19  
; Sequence 19, Application US/09740002  
; Patent No. US20020001798A1  
; GENERAL INFORMATION:  
; APPLICANT: BRAMS, PETER  
; APPLICANT: MORROW, PHILLIP  
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF  
; FILE REFERENCE: 037003-0275759  
; CURRENT APPLICATION NUMBER: US/09/740,002  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/335,697  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 08/488,376  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 1428  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1425)  
US-09-740-002-19

Query Match 78.6%; Score 1125.2; DB 10; Length 1428;  
Best Local Similarity 88.6%; Pred. No. 5.3e-302;  
Matches 1256; Conservative 0; Mismatches 153; Indels 9; Gaps 3;

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QY 77 CGGGCCAGGACTGGTGAAGCTTCCGAGACCTGTCCCTCACCTGCGCTGTCTGTGGT 136  
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QY 137 GCTC---CATCAGCGGTGTATGGCTGGGCTGGATCCGACGCCGCCAGGGAAGGGGC 193  
Db 137 TCTCACTCAGCACGAGGAATGAGTGTAACTGGATCGTTCAGCCCCCAGGGAAGGCC 196  
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QY 254 AGAGTCAAGTCAACATTTTCAACAGACACAGTCCAGAACACAGTTCTCCCTGAAGCTGAAC 313  
Db 254 AGACTAGGCTCAGCATCTTCAAGGACACCTCCAAAACACAGGTGGTCTCTCAGAATGACCA 313  
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QY 434 CCTCAGCTAGCACAAAGGGCCCATCGGTCTTCCCTCCCTGGCACCCTCTCCAAAGACACCT 493  
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QY 554 TGTCTGTAACCTCAGCGGCCCTGACCGAGGGGGTGCACACCTTCCCGGCTGTCTACAGT 613  
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QY 794 GGGACCTCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGA 853  
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QY 854 CCCCTGAGGTCAATGCTGTGTGTGAGCGTGAGCCAGAGACCTCTGAGGTCAAGTTCA 913  
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Db 971 ACACAGCACCTACCGTGTGTGTGAGCGTCTCTCACCGTCTGCACAGGACTGGCTGAATG 1030  
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QY 1154 ATGAGCTGACCAAGAACAGGCTGAGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1213  
Db 1151 ATGAGCTGACCAAGAACAGGCTGAGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1210  
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Db 1271 CGGTGCTGAGCTCCGAGCGCTCTCTCTCTCTCTACAGCAAGCTCACCGTGGACAGAGCA 1330









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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:26:38 ; Search time 81.6185 Seconds.  
(without alignments)  
5376.898 Million cell updates/sec

Title: US-09-576-424-11  
Perfect score: 1431  
Sequence: 1 atgaacacctgtgttctt.....ccctgtctcgggtaataga 1431

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/5A COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5B COMB.seq:\*
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- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	3	US-08-487-550-11
2	1315.8	91.9	1431	3	US-08-487-550-3
3	1276.4	89.2	1567	3	US-09-049-672A-17
4	1213.6	84.8	1418	4	US-08-793-450-7
5	1181	82.5	1404	3	US-08-523-894-7
6	1177.8	82.3	1404	3	US-08-523-894-11
7	1176.2	82.2	1404	3	US-08-523-894-9
8	1134.8	79.3	1428	1	US-08-488-376-17
9	1134.8	79.3	1428	2	US-08-634-223-17
10	1134.8	79.3	1428	2	US-08-634-223-17
11	1134.8	79.3	1428	2	US-08-634-400-17
12	1134.8	79.3	1428	2	US-08-635-878-17
13	1134.8	79.3	1428	2	US-08-770-057-17
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17	1125.2	78.6	1428	2	US-08-634-223-19
18	1125.2	78.6	1428	2	US-08-634-224-19
19	1125.2	78.6	1428	2	US-08-634-400-19
20	1125.2	78.6	1428	2	US-08-635-878-19
21	1125.2	78.6	1428	2	US-08-770-057-19
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23	1125.2	78.6	1428	4	US-09-335-697B-19
24	1121.2	78.4	1617	2	US-08-378-939-9
25	1118	78.1	19040	4	US-09-343-485A-3
26	1112.4	77.7	1437	3	US-08-487-550-7
27	1107.8	77.4	1576	1	US-08-157-101A-6

Query Match 100.0%; Score 1431; DB 3; Length 1431;

ALIGNMENTS

RESULT 1  
US-08-487-550-11  
; Sequence 11, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1431 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1431  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 1..1431  
; US-08-487-550-11

28 1102.2 77.0 6557 1 US-08-286-740-3 Sequence 3, Appli  
29 1102.2 77.0 6557 5 PCT-US95-09576-3 Sequence 3, Appli  
30 1097.8 76.7 1350 1 US-08-157-101A-9 Sequence 9, Appli  
31 1096.6 76.6 9209 1 US-08-149-099C-3 Sequence 3, Appli  
32 1096.6 76.6 9209 1 US-08-476-275-2 Sequence 2, Appli  
33 1096.6 76.6 9209 4 US-08-478-967A-3 Sequence 3, Appli  
34 1096.6 76.6 9209 2 US-08-475-815B-3 Sequence 3, Appli  
35 1096.6 76.6 18986 2 US-08-813-866-2 Sequence 2, Appli  
36 1096.6 76.6 18986 2 US-09-023-715-2 Sequence 2, Appli  
37 1096.6 76.6 18986 4 US-09-343-485A-2 Sequence 2, Appli  
38 1093.8 76.4 8120 3 US-09-027-449-68 Sequence 68, Appli  
39 1093.8 76.4 8120 3 US-09-026-985-68 Sequence 68, Appli  
40 1093.8 76.4 8120 4 US-09-121-952A-68 Sequence 68, Appli  
41 1093.8 76.4 8120 4 US-09-234-340A-68 Sequence 68, Appli  
42 1069 74.7 1655 3 US-09-049-672A-21 Sequence 21, Appli  
43 1051.2 73.5 6285 1 US-08-467-420A-49 Sequence 49, Appli  
44 1051.2 73.5 6285 1 US-08-470-110A-49 Sequence 49, Appli  
45 1051.2 73.5 6285 1 US-08-667-769A-49 Sequence 49, Appli



**LOCATION:** 1..1431  
**US-08-487-550-3**

	Query Match	91.9%	Score 1315,8;	DB 3;	Length 1431;
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QY	61	GTGCAGCTGCAGAGTGGGCCAGGACTGGTGAAGCCTTCGAGAGACCTGTCTCCCTCAC	120		
DB	61	GTGAAGCTGCAGAGTGGGCCGAAGGACTTCTGCAGCCTTCGAGAGACCTGTCTCCGAC	120		
QY	121	TGCGCTGTCTCTGTGGCTCCATCAGCGGTGGTTATGGCTGGGCTCGATCCGGCAGCCC	180		
DB	121	TGCGTTGTCTCTGTGGCTCCATCAGCGGTACTACTACTGGACCTCGATCCGGCAGAC	180		
QY	181	CCAGGAAGGGCTGGAGTGGATGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC	240		
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QY	241	AACCCCTCCTCAAGAGTCAAGTCAACATTTCAACAGACAGTCCAAAGAACAGTTCTCC	300		
DB	241	AATCCCTCCTCAAGAGTCAGTCAACATTTCAAAGACAGTCCAAAGAACAGTTCTTC	300		
QY	301	CTGAAGCTGAATCTATGACCGCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT	360		
DB	301	CTGAATCTGAATCTGTGACCGGACCGGACACGGCCGTCTATTACTGTGGAGAGCCCT	360		
QY	361	CTTTTTTCAGTTGGAAATGGTTTCAACAACTGGTTCGATGCTGGGGCCCGGGAGTC	420		
DB	361	CGCCCTGATTGCACAACATTTGTTATGGCGGTGGGTGATGCTGGGGCCCGGGAGAC	420		
QY	421	CTGGTCAACGTTCTCCTCAGCTAGCAACAAAGGGCCCATCGGTCTTCCCTTGGACACCTCC	480		
DB	421	CTGGTCAACGTTCTCCTCAGCTAGCACAAAGGGCCCATCGGTCTTCCCTTGGACACCTCC	480		
QY	481	TCCAAGAGCACTCTGGGGGACACAGCGGCCCTGGGGCTCTGGTCAAGGACTACTTCCCC	540		
DB	481	TCCAAGAGCACTCTGGGGGACACAGCGGCCCTGGGGCTCTGGTCAAGGACTACTTCCCC	540		
QY	541	GAAACCGGTGACGGTGTGCTGGAATCTCAGGGGCCCTGACAGCGCGGTGCACACCTCCCG	600		
DB	541	GAAACCGGTGACGGTGTGCTGGAATCTCAGGGGCCCTGACAGCGCGGTGCACACCTCCCG	600		
QY	601	GCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGC	660		
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DB	661	AGCTTGGGACCCAGACCTACATCTCAACGTGAATCACAAAGCCACGACCAACCAAGGTG	720		
QY	721	GACAAGAAAGCAGAGCCCAATCTTGTGACAAAACCTCACATGCCCAACCGTGCACGCA	780		
DB	721	GACAAGAAAGCAGAGCCCAATCTTGTGACAAAACCTCACATGCCCAACCGTGCACGCA	780		
QY	781	CCTGAACTCTGGGGGACCGTCACTCTTCTTCTTCCCCCAAAACCCAAAGGACACCTC	840		
DB	781	CCTGAACTCTGGGGGACCGTCACTCTTCTTCTTCCCCCAAAACCCAAAGGACACCTC	840		
QY	841	ATCATCTCCCGGACCCCTGAGGTACATCGTGGTGGACGTGGACGCGCAGAGACCTT	900		
DB	841	ATCATCTCCCGGACCCCTGAGGTACATCGTGGTGGACGTGGACGCGCAGAGACCTT	900		
QY	901	GAGGTCAAGTTCAACTGTACGTGGACCGGCTGGAGGTGATATATGCAAGACAAAGCCG	960		
DB	901	GAGGTCAAGTTCAACTGTACGTGGACCGGCTGGAGGTGATATATGCAAGACAAAGCCG	960		
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Db	961	CGGAGAGCAGTACAAACAGCAGTACCGGTGTGGTCTCAGCGTCTCTACCGGTCTCTGCACCAG	1020
Qy	1021	GACTGGCTGAATGGCAAGAGTAAAGTGTCAAGGTCTTCCAAACAAAGAGCCCTCCAGAGCCCCC	1080
Db	1021	GACTGGCTGAATGGCAAGAGTAAAGTGTCAAGGTCTTCCAAACAAAGAGCCCTCCAGAGCCCCC	1080
Qy	1081	ATCGAGAAAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCCCTG	1140
Db	1081	ATCGAGAAAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCCCTG	1140
Qy	1141	CCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCCTGGTCAAAAGGC	1200
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Qy	1201	TTCTATCCAGCACATCGCGGTGGAGTGGGAGAGCAATGGGAGCCGAGAGAACCAACTAC	1260
Db	1201	TTCTATCCAGCACATCGCGGTGGAGTGGGAGAGCAATGGGAGCCGAGAGAACCAACTAC	1260
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Qy	1321	GTGGACAGACAGGTGGCAGCGAGGGGAAAGCTTCTCATGCTCCGTTGATGCATGAGCT	1380
Db	1321	GTGGACAGACAGGTGGCAGCGAGGGGAAAGCTTCTCATGCTCCGTTGATGCATGAGCT	1380
Qy	1381	CTGCACAAACACTACACGACGAAGAGGCTCTCCCTGTCTCCGGGTAATGA	1431
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RESULT 3  
 US-09-049-672A-17  
 ; Sequence 17, Application US/09049672A  
 ; Patent No. 6135941  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Baughn, Mariah R.  
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/049,672A  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cerrone, Michael C  
 ; REGISTRATION NUMBER: 39,132  
 ; REFERENCE/DOCKET NUMBER: PF-0497 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166





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; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1418
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; NAME/KEY: sig_peptide
; LOCATION: 1..57
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..1418
; OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY
; OTHER INFORMATION: CHAIN"
; US-08-793-450-7

Query Match      84.8%; Score 1213.6; DB 4; Length 1418;
Best Local Similarity 92.5%; Pred. No. 1.8e-283;
Matches 1312; Conservative 0; Mismatches 94; Indels 12; Gaps 3

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DB      13  TGTATCATCTCTCTCTGGTAGCACAGTACAGTGTCCATCCAGGTCCAACCTGGAG 72

QY      73  GAGTCGGGCCCAGGACTGGTGAAGCCTTTGGGAGACCTGTTCCTCACCTGCGCTGTCTCT 132
DB      73  CAGTGGGGCGCAGGACTGTTGAAGCCTTTGGGAGACCTGTTCCTCACCTGCACTGTCTAT 132

QY      133 GGTGGCTCCATCAGGGTGGTTATGGCTGGGGCTGGATCCGCGAGCCCCCAGGGAAGGG 192
DB      133 GGTGGGTCTTTCA---GTGGTTACTACTGGAGCTGGATCCGCGAGCCCCCAGGGAAGGG 189

QY      193 CTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTACAACCCCTCCCTC 252
DB      190 CTGGAGTGGATTGGGGAATC---AATCATAGTGAAGCACCACCTACAAACCGTCCCTC 246

QY      253 AAGAGTCMAGTCAACATTTCACAGACACGTCCAAAGAACCAAGTTCTCCCTGAAGCTGAAC 312
DB      247 AAGAGTCGAGTCACCATATCAGTAGACACGTCCAAAGAACCAAGTTCTCCCTGAAACTGAAC 306

QY      313 TCTATGACCGCGCGGACACGCGCTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTT 372
DB      307 TCTGTGACCGCGCGGACACGCGTGTATTACTGTGTGAGGCGCCGAGTATAAA--- 363

QY      373 GTTGGAAATGGTTTACAAACACTGGTTCGATGTCGGGGCCGCGGAGTCTCGTGTACCCGTC 432
DB      364 ---TGGAGATATATGGGGACTGGTTTCGACCCCTGGGCGCAAGGTACCACTGTCAACCGTC 420

QY      433 TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGGCAACCTCTCTCCAAGAGCAC 492
DB      421 TCCTCAGGCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGGCAACCTCTCTCCAAGAGCAC 480

QY      493 TCTGGGGGCACAGCGGCCCTGGGCTCGCTGGTTCGAAGGACTACTTCCCGGAACCGGTGAG 552
DB      481 TCTGGGGGCACAGCGGCCCTTGGGCTGCTTGGTCAAGGACTACTTCCCGGAACCGGTGAG 540

QY      553 GTGTCGTGGAACTCAGGCGCCCTGCACCAAGCGCGGTGCACACCTTCCCGGCTGTCTCTACAG 612
DB      541 GTGTCGTGGAACTCAGGCGCCCTGCACCAAGCGCGGTGCACACCTTCCCGGCTGTCTCTACAG 600

QY      613 TCCTCAGGACTCTACTCCTCAGACAGCGTGTGACCGTGTGCCCTTCAGAGCTGTGGGAC 672
DB      601 TCCTCAGGACTCTACTCCTCAGACAGCGTGTGACCGTGTGCCCTTCAGAGCTGTGGGAC 660

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Qy	673	CAGACCTACATCTGCAACGTGAATCTCAAGACCCAGCAACACCAAGGTGGACAAAGAAGCA	732
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Qy	733	GAGCCCAAAATCTTGTGACAAAACCTACACATGCCACCGTGCACGACCTGAACTCCCTG	792
Db	721	GAGCCCAAAATCTTGTGACAAAACCTACAGACATGCCACCGTGCACGACCTGAACTCCCTG	780
Qy	793	GGGGGACCGGTCACTCTTCTTCCCGCCCAAAACCCAAAGGACACACCTCATGTCTCCCGG	852
Db	781	GGGGGACCGGTCACTCTTCTTCCCGCCCAAAACCCAAAGGACACACCTCATGTCTCCCGG	840
Qy	853	ACCCCTGAGGTACATGCTGT	912
Db	841	ACCCCTGAGGTACATGCTGT	900
Qy	913	AATCGT	972
Db	901	AATCGT	960
Qy	973	TACAAACAGCACGTACCGT	1032
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Qy	1033	GGCAAGGAGTACAAAGTGTGAAGTGTCTCAACAAAGCCCTCCAGCCCCCATTCGAGAAAACC	1092
Db	1021	GGCAAGGAGTACAAAGTGTGAAGTGTCTCAACAAAGCCCTCCAGCCCCCATTCGAGAAAACC	1080
Qy	1093	ATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGG	1152
Db	1081	ATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGG	1140
Qy	1153	GATGAGTGTACCAAGAACAGGTGTGACCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	1212
Db	1141	GATGAGTGTACCAAGAACAGGTGTGACCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	1200
Qy	1213	GACATCCCGTGTGAGTGGGAGAGCAATGGGACGCGGAGAACAACTACAAGACCAACGCT	1272
Db	1201	GACATCCCGTGTGAGTGGGAGAGCAATGGGACGCGGAGAACAACTACAAGACCAACGCT	1260
Qy	1273	CCCGTGTGTGATCCGACCGCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1332
Db	1261	CCCGTGTGTGATCCGACCGCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1320
Qy	1333	AGGTGTGAGCAGGAGGAAAGCTTCTCTCATGTCTCGTGTATGATGAGGCTCTGCAACACCCAC	1392
Db	1321	AGGTGTGAGCAGGAGGAAAGCTTCTCTCATGTCTCGTGTATGATGAGGCTCTGCAACACCCAC	1380
Qy	1393	TACACGAGAAGAGCTCTTCT	1430
Db	1381	TACACGAGAAGAGCTCTTCT	1418

RESULT 5

US-08-523-894-7

; Sequence 7, Application US/08523894

; Patent No. 6136310

; GENERAL INFORMATION:

; APPLICANT: Hanna, Nabil

; APPLICANT: Newman, Roland A.

; APPLICANT: Reff, Mitchell E.

; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

; TITLE OF INVENTION: Therapy

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314-3187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

## RESULT 5

US-08-523-894-7

; Sequence 7, Application US/08523894

; Patent No. 6136310

**; GENERAL INFORMATION:**

APPLICANT: Hanna, Nabila

APPLICANT: Newman, Roland A.

APPLICANT: REIL, MITCHELL E.  
TITLE OF INVENTION: RECEIPT

TITLE OF INVENTION:	RECOMBINATION
TITLE OF INVENTION:	Therapy

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER &amp; MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA  
COUNTRY: "03

;  
 COUNTRY: USA  
 ZTR. 32314-3197

; ZIP: 22314-3107  
; COMPITER READABLE FORM:

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MEDIUM TYPE: Floppy disk

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11-11-11

























QY 494 CTGGGGGACACGGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGAAACCGGTGACGG 553  
Db |||||  
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Db |||||  
QY 554 TGTCTGTGAACCTCAGCGGCCCTGACAGCGGGGTGCACACCTTCCCGGCTGCTTACAGT 613  
Db |||||  
QY 551 TGTCTGTGAACCTCAGCGGCCCTGACAGCGGGGTGCACACCTTCCCGGCTGCTTACAGT 610  
Db |||||  
QY 614 CCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 673  
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QY 611 CCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 670  
Db |||||  
QY 674 AGACCTACATCTGCAAGCTGAATCAAGCCCGAGCAACACCAAGGTGGAACAAGAAAGCAG 733  
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QY 671 AGACCTACATCTGCAAGCTGAATCAAGCCCGAGCAACACCAAGGTGGAACAAGAAAGCAG 730  
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